

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus.n2p model

Run on: August 22, 2003, 13:47:31 ; Search time 103 Seconds
(without alignments)
4786.454 Million cell updates/sec

Title: US-09-745-506-74

Perfect score: 2789
Sequence: 1 GTGATGTGATCTGTGCTCTCTCTTACTTAACTTCAA 1553

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1107863 segs, 158726573 residues

Total number of hits satisfying chosen parameters: 2215726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0-UNITS=bits-START=1-END=1-MATRIX=blomsu62-TRANS=human40.cd1
-LIST=45-DOCALLION=200-THR_SCORE=pcr-THR_MAX=100-THR_MIN=0-ALIGN=15
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-USER=US09745506.GCN.1.1.137.etrnat.22082003.132709.10724-NCPU=6-ICPU=3
-NO_MAMP-LANG=ENGERY-NEG_SCORES=0-WAIT-DSPBLOCK=100-LONGLOG
-DEV_TIMEOUT=120-WARN_TIMEOUT=30-THREADS=1-XGAPOP=10-XGAPEXT=0.5-FGAPOP=6
-FGAPEXT=7-YGAPOP=10-YGAPEXT=0.5-DELOP=6-DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1896	68.0	383	22 AAM88085	Human immune/haema
2	1890	67.8	377	22 AAU27744	Human full-length
3	1799	64.5	350	22 AAC81361	Human AFP protein
4	1799	64.5	350	22 AAB94571	Human protein sequ
5	1743.5	62.5	351	22 AAB60653	Human gene express
6	1209	43.3	247	23 AAB08182	Human protein kina
7	599	21.5	146	22 AAB07916	Human cortig polyP
8	578	20.7	288	22 AAB60530	Drosophila melano
9	518	18.6	110	22 AAB620985	Novel human diago
10	366	13.1	68	22 AAB62473	Human liver peptid
11	366	13.1	68	22 AAB32385	Peptide #5036 enco
12	366	13.1	68	22 AAB37667	Peptide #5173 enco
13	366	13.1	68	22 AAM58295	Human brain expres
14	366	13.1	68	22 AAM18609	Peptide #5043 enco
15	366	13.1	68	22 AAM06178	Peptide #4860 enco
16	330	11.8	79	22 AAU21467	Human novel foetal
17	314.5	11.3	70	22 AAB620982	Novel human diago
18	305	10.9	367	23 AAB38833	Staphylococcus epi
19	296	10.6	360	22 AAC82538	S. epidermidis ope
20	289.5	10.4	403	22 AAU54649	Propionibacterium
21	249	8.9	376	22 AAC82506	S. epidermidis ope
22	240	8.6	373	23 AAB847970	Listeria monocytog
23	230	8.2	380	22 AAC92158	C. glutamicum prote
24	230	8.2	380	22 AAB79495	Corynebacterium q1
25	216.5	7.8	379	24 AAB57497	Mycobacterium tube
26	216	7.7	264	23 AAB26738	Streptococcus poly
27	203.5	7.3	265	24 AABU02074	S. pneumoniae type
28	190	6.8	252	22 AABU02074	Human immune/haema
29	187.5	6.7	256	23 AAB54389	Lactococcus lactis
30	174	6.2	262	23 AAB30359	Streptococcus poly
31	174	6.2	263	23 AAB26737	Streptococcus poly
32	157.5	5.6	244	22 AAC81950	S. epidermidis ope
33	142	5.1	74	22 AAB620984	Novel human diago
34	120	4.3	316	23 AAM49408	Escherichia coli r
35	115	4.2	22	22 AAB620983	Novel human diago
36	109.5	3.9	733	22 AAU18289	Human endocrine po
37	107	3.9	961	23 AAU80188	Human TSP1 domain
38	107	3.9	966	23 AAU80188	Human TSP1 domain
39	105.5	3.8	3829	22 AAB97819	Human spastin prot
40	105.5	3.8	3829	22 AAB97823	Human spastin prot
41	105	3.8	644	14 AAB38751	Human mutated spas
42	104.5	3.7	473	23 AAB61562	DEL protein. Anti
43	104.5	3.7	473	23 AAB61562	High growth methan
44	103.5	3.7	3830	22 AAB97820	Methylomonas glyco
45	103	3.7	673	20 AAB93593	Mouse spastin prot
					Human kidney amino

ALIGNMENTS

RESULT 1

AAAM88085

AAAM88085 standard; Protein: 383 AA.

07-NOV-2001 (first entry)

Human immune/haematopoietic antigen SEQ ID NO:15678.

Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

cytostatic; gene therapy; vaccine; metastasis.

Homo sapiens.

WO200157182-A2.

09-AUG-2001.

XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Claim 11: SEQ ID NO 15678; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX

SQ Sequence 383 AA:

Alignment Scores:
Pred. No.: 6,55e-181 Length: 383
Score: 1896.00 Matches: 370
Percent Similarity: 99.73% Conservative: 1
Best Local Similarity: 99.73% Mismatches: 0
Query Match: 67,98% Indels: 0
DB: 22 Gaps: 0

US-09-745-506-74 (1-1553) x AAM88085 (1-383)

OY 182 AGATGAGTCCCGACGACGATCCGGTTGTAGATCCCTGATCTGCAATTCCTCCGCTCC 241
DB 13 ArgProValProThrThrValAlaArgPheValAspSerLeuIleCysHisSerHisArgSer 32
OY 242 TTCATGAGATTGAAGGCTCTCTTCTTCTTCTGATGACTTGGCATCCCTCTGTTGGCT 301
DB 33 PheMetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAla 52
OY 302 GAGAGTGGGACAAATTTGATGATTCGTGGGAACCAAGCCACCAATACCTGTAATACA 361
DB 53 GluSerTrpAspAsnValGlyLeuLeuValGluProSerProToroHisThrValAsnTrp 72
OY 362 CTCTTCCTGACCAATGACCTGACTGAGGAAGTATGAGAGAGGTGTCGCAAAAGAGGCA 421
DB 73 LeuPheLeuThrAsnAspLeuThrGluGluValMetGluValLeuGlnLysLysAla 92
OY 422 GACCTCATCTCTCTTACCATCCGCTATCTCCAGCCATGAAGGCATTAACCTGGAAC 481
DB 93 AspLeuIleLeuSerTrpHisProProlePheArgProMetLysArgIleThrTrpAsn 112
OY 482 ACATGGAAGGAGCGCTGCTGATCCGGCTTGGGAAGAGTCCGATCTACTCTCCCT 541
DB 113 ThrTrpLysGluArgLeuValIleArgAlaLeuGlnAsnArgValGlyIleTrpSerPro 132
OY 542 CATACAGCCTATGATCTCGCCGCCAGGCGTCACAACTGATGGCTAAAGGCGCTGGA 601
DB 133 HisThrAlaLysAspAlaLysAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGly 152
OY 602 GCTTGACCTCCAGGCCCATATCATCTCCAAAGCTCCCAACTACCTACAGAGGAAC 661
DB 153 AlaCysThrSerArgProIleHisProSerLysAlaLysAsnTrpProThrGluGlyAsn 172
OY 662 CACCGAGTGAATTAAGCTTAATCACTACCAAGAGCTGGAACAATCATGCTGGAAG 721
DB 173 HisArgValGluPheAsnValAsnTrpHisGlnAspLeuAspLysValMetSerAlaVal 192

OY 722 AAGAATGACGCGTCTTCTGTCACTTCTTTCTGTAGAGTGGTAAATGAGACA 781
DB 193 LysGlyIleAspLysValSerValIleThrSerSerAlaArgThrGlnGluGln 212
OY 782 ACAGGATTAATGTAATGTACTACAGAACGCTTTGATGAGGTGATATTTCTTCC 841
DB 213 ThrArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetClnValValAspPheLeuSer 232
OY 842 CGGAACAAACACTTTATTCAGAGACGGAATCTGTCACTGGAGAACGCTTGTCTTA 901
DB 233 ArgAsnLysGlnLeuTrpGlnLysTrpGlnIleLeuSerLeuLysProLeuLeu 252
OY 902 CATACGGAATGAGCGGTTATGACACACTGATGAATCTGTCTCCGCGCAACATGAT 961
DB 253 HisThrGlyMetCylArgLeuCysThrIleAspGluSerValSerLeuAlaThrMetIle 272
OY 962 GATCGAATAAAGAACACCTAAACATATTCATATTCGCTTACCCCTGGGGTGGGAGA 1021
DB 273 AspArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValArg 292
OY 1022 ACCTTAGAGCTCAAGTCAAGACGCGCCCTGTGCTGTCTGGAGACAGCTTCTG 1081
DB 293 ThrLeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerValLeu 312
OY 1082 CAGGAGTGGAGGCTGACCTTACCTCACAGGTGAGATGCCATCATGATCTTGGAT 1141
DB 313 GlnGlyValGlnLysAlaAspLeuTrpLeuThrGlyGluMetSerHisAspThrLeuAsp 332
OY 1142 GCTGCTTCCCAAGGAATTAATGTCATCTGTGACACAGCAACACTGAGAGGCTTT 1201
DB 333 AlaAlaSerGlnGlyIleAsnValIleLeuCysGlnHisSerAsnThrGluArgLysPhe 352
OY 1202 CTTCCTGACCTTGAAGATATGCTGATTCACACTTGGAGAAATGAATATATTCCTA 1261
DB 353 LeuSerAspLeuArgAspMetLeuAspSerHisLeuGlnLysIleAsnIleLeu 372
OY 1262 TCAGAGACTGACAGGACCTCTTCAGGTGTA 1294
DB 373 SerGluThrAspArgAspProLeuGlnValVal 383

RESULT 2
AAU27744
AAU27744 standard; Protein: 377 AA.
XX
AC AAU27744:
XX
DE Human full-length polypeptide sequence #69.
XX
KW Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukemia;
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW nervous system disorder; inflammatory disorder; cell differentiation;
KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
KW cytostatic; antihermetic; antiarthritic; vulnereary; inflammatory;
KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
KW neuroprotective; osteopathic; antidiabetic; antistimatic; antiallergic;
KW immunostimulant; analgesic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200164834-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-0504926.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
PR 17-JUN-2000; 2000US-0597707.
PR 14-JUL-2000; 2000US-0616807.

PR 19-SEP-2000; 2000US-0664641.
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
PI Drmanac R;
XX WPI; 2001-589862/66.
DR N-PSDB; AAS44644.
XX
PT Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis, treatment of
PT cancer, neurological, inflammatory disorders and for use in arrays for
PT detection
XX
XX Claim 10; SEQ ID NO 241; 153pp; English.
XX
CC Sequences AAU27676-AAU28019 represent full-length polypeptides and
CC contig polypeptides of the invention. The proteins and their associated
CC DNA sequences are useful for the treatment, diagnosis and prevention of
CC various types of disorder in a mammalian subject such as a human, dog,
CC monkey, mouse, hamster or rat. The disorders include cancers such as
CC leukemia, lymphoma and neuroblastoma, autoimmune disorders such as
CC multiple sclerosis, connective tissue disease, rheumatoid arthritis,
CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's
CC disease, ischemia-reperfusion injury, shock, sepsis and inflammatory
CC bowel disease. The sequences exhibit activity relating to angiogenesis,
CC cell proliferation, cell differentiation, stem cell growth factor,
CC activin or inhibin. Therefore, they can be used to manipulate stem cells
CC in culture to give rise to neuroepithelial cells that can be used to
CC augment or replace cells damaged by illness, accidental damage or genetic
CC disorders. The sequences may also be used for regeneration of bone,
CC cartilage, tendons and ligaments and in tissue repair and burn healing.
CC Note: Some sequences for this patent did not form part of the printed
CC specification, but were obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 377 AA;
SQ
Alignment Scores:
Pred. No.: 2.6e-180 Length: 377
Score: 1890.00 Matches: 369
Percent Similarity: 99.46% Conservative: 0
Best Local Similarity: 99.46% Mismatches: 2
Query Match: 67.77% Indels: 0
DB: 22 Gaps: 0
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DB 7 ArgprovalProthThrValAlaRheValAspSerLeuIleCysAsnSerSerArgSer 26
QY 242 TTCATGATTTGAAGGCTCTCTTCTCTTCTGAAATGACTTGCATCCCTCTGTTCT 301
DB 27 PhenetaspleuylsAlaLeuLeuSerSerLeuAsnAspRheAlaSerLeuSerRheAla 46
QY 302 GAGAGTTGGACATGTTGATTTACTGTGTGAACCAAGCCCAACATCTGTAATACA 361
DB 47 GluSerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThr 66
QY 362 CTCCTCCGACCAATGACCTGACTAGAGATGAGAGAGAGAGCTCTCCAAAAGAGCA 421
DB 67 LeuphLeuThrAsnAspLeuThrGluValMetGluGluValLeuGlnLysLysAla 86
QY 422 GACCTCATCTCTCTACATCCGCTATCTCCGACCATGAAGCATACCTGAGAAC 481
DB 87 AspLeuIleLeuSerTyrHisProProIlePheAlaGlyPheAlaGlyIleThrTrpAsn 106

QY 482 ACATGAGAGAGCGCCGCTGATCCGGCTCTGGAGAAAGAGTCTATCTCTCT 541
DB 107 ThrTrpLysGluThrGluValAlaIleArgAlaLeuGlnAsnArgValGlyIleTyrSerPro 126
QY 542 CATACAGCTTATGATGCTGGCGCCACAGGCGTCAACACTGTTGGCTAAAGGCTTGA 601
DB 127 HisThrAlaThrAspAlaAlaProGlnGlyValAsnAsnThrPheAlaLysGlyLeuGly 146
QY 602 GCTTGTACCTCCAGGCGCCATACATCTCTCCAAAGCTCCCAACTCCCTACAGGGGAAAC 661
DB 147 AlaCysThrSerAlaGProIleHisProSerLysAlaProAsnTrpProThrGluLysAsn 166
QY 662 CACGAGTAGAATTCACAGTTAACTACACCCAAAGCTGGACAAAGTCAATGCTGCAGTG 721
DB 167 HisArgValGluPheAsnValAsnTrpThrGlnAspLeuAsnLysValMetSerAlaVal 186
QY 722 AAAGAAATTCAGGCTGTTTCTGTACATCTCTTCTCTGCTAGAGCTGTAATGAGAAACA 781
DB 187 LysGlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGln 206
QY 782 ACAGGATTAATTCGATTTGACTCAGAGGCTTGAAGGCTGATGATTTCTTCC 841
DB 207 ThrArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValAlaAspPheLeuSer 226
QY 842 CGGAACAACAACCTTTATCAGAGAGCGAAATCTGTCACTGAGAGAACCTTTGCTCTTA 901
DB 227 ArgAsnLysGlnLeuThrGlnLysThrGluIleLeuSerLeuGlnLysProLeuLeuLeu 246
QY 902 CATACGTAATGAGAGGCTTATGCACACTGATGATCTGTCTCCCTGGACACATGAT 961
DB 247 HisThrGlyMetGlyArgLeuLysThrLeuAspGlnSerValSerLeuAlaThrMetIle 266
QY 962 GATCGAATTAATAAGACACTTAAACTATCTATATTCCTTACAGCCCTGGGGTGGAGAGA 1021
DB 267 AspArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArg 286
QY 1022 ACCTTAGAGTTCAGTCAAGTCAAGTGGCGCTGTGTCTGTCTGCTGTTCTGGAGACAGCTTCTG 1081
DB 287 ThrLeuGlnSerGlnValLysValValAlaLeuLysAlaGlySerValLeu 306
QY 1082 CAGGCTGTGAGGCTGACCTTTTACTCTACAGAGTGAAGTCCCATCATGATCTTGAT 1141
DB 307 GlnGlyValGlnAlaAspLeuThrLeuThrGlyGlnMetSerHisHisAspIleLeuAsp 326
QY 1142 GCTGCTTCCCAAGGAATTAATGTCATCTGTGTGAACACAGACACTGAAGAGAGCTTT 1201
DB 327 AlaAlaSerGlnGlyIleAsnValIleLeuLysGlnHisSerAsnThrGluArgGlyPhe 346
QY 1202 CTTTCTGACCTTCGATATGCTGTGATTTCTCACTTGGAGAAATTAATTAATTCCTTA 1261
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QY 1262 TCAGAGACTGACAGGAGCCCTTTCAGGTGGA 1294
DB 367 SerGluThrAspArgAspProLeuGlnValVal 377
RESULT 3
AAAG81361
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AC AAAG81361;
XX
XX 10-SEP-2001 (first entry)
DE Human AFP protein sequence SEQ ID NO: 240.
XX
XX Human; secreted protein; secretion: bacterial cell; fungal cell;
KW eukaryotic cell; fusion protein; maltose binding protein;
KW immunoglobulin constant region; polynucleotide tag.
XX Homo sapiens.
XX
PN WO200129221-A2.

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XX 26-APR-2001.
PD 20-OCT-2000; 2000MO-US29052.
PR 20-OCT-1999; 99US-0160712.
XX (ZYMO) ZYMOGENETICS INC.
PI Conklin DC, Yee DP;
XX MPI; 2001-300340/31.
DR N-PSDB; AAH52212.
XX Isolated polypeptide for directing secretion of proteins of interest
PT from a host cell including, e.g. bacteria, includes contiguous amino
XX acid residues of polypeptide with specified amino acids
PS Claim 1; Page 424-425; 617pp; English.
XX
XX AAH52093 to AAH52303 encode the human secreted proteins given in AAH521242
XX to AAH521453. The secreted proteins can be used for directing the
XX secretion of proteins of interest from a host cell including bacteria,
XX fungal cells, and cultured higher eukaryotic cells. The present invention
XX also describes fusion proteins, where a secreted protein of the invention
XX is operably linked via a peptide bond or peptide linker to a second
XX protein selected from the group consisting of maltose binding protein,
XX an immunoglobulin constant region, a polystyidine tag and a peptide
XX given in AAH521453.
XX
XX Sequence 350 AA;
XX
XX Alignment Scores:
XX Pred. No.: 3,36e-171 Length: 350
XX Score: 1799.00 Matches: 350
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 64.50% Indels: 0
XX DB: 22 Gaps: 0
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XX US-09-745-506-74 (1-1553) x AAH81361 (1-350)
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XX 245 ATGGATTGGAAGGCTCTCTTCTTCCTGAATGACTTTCAGCCCTCTGTTGCTGAG 304
XX 1 MetasprenulysalaleuleuserSerleuasnaphelaSerleuSerphelaIglu 20
XX
XX 305 AGTTGGACAATGTTGGATTACTGTTGGAACCAAGCCACACATCTGTAATACACTC 364
XX 21 SerTTPAspAsnValGlyLeuLeuValGluProSerProHistiThrValAsnThrLeu 40
XX
XX 365 TTGCTGACCAATGACCGACTGAGAGAGTATGAGAGAGTGGCTGGCAAAAGAGCGAC 424
XX 41 PhleuThrAsnAspLeuThrGluValMetIuValLeuGlnLysAlaAsp 60
XX
XX 425 CTCATTCTCTACATCCGCGCTATCTTCGACCCATGAGAGCGCATACCTGGAGACA 484
XX 61 LeuileuSerThrHisProProllePheArgProMetLysArgIleHnThrAsnThr 80
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XX 485 TGGAGAGAGCGCGCTGGTATCCGGGCTGTGAGAACAGAGCTGGTATCTCTCAT 544
XX 81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
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XX 545 ACAGCGCATGATGCTGGCGCCGAGGGGCTGACAAAGCGTGGTAAGGCTTGGAGCT 604
XX 101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
XX
XX 605 TGTACCTCCAGGCGCCATACATCTCTCCAAAGCTCCCAACTACCTACAGAGGAGAACAC 664
XX 121 CysThrSerArgProIleHisProSerLysAlaProAsnTrpProHnThrGluGlyAsnHis 140
XX
XX 665 CGAGTGAATTCACGTTAACTACACCCAGACCTGGACAAAGTCACTGTCTGCAGTAAA 724
XX 141 ArgValGluIubAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160

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QY 725 GGAATGACGCGTCTTCTGTCACCTTTCTTCTCTGACAGCTGTAATGAGAACAAACA 784
DB 161 GlyIleAspGlyValSerValThrSerPheSerIleArgThrGlyAsnGluGlnThr 180
QY 785 CGGATTATATCGAATTTACTACAGAGCGTTTGAAGAGGTGAGATTTTCTTCCCGG 844
DB 181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetIleValAlaAspPheLeuSerArg 200
QY 845 AACAAACAACTTTATTCAGAAAGACGAAATTCCTGTCACTGAGAGAACCTTGTCTACAT 904
DB 201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGlnLysProLeuLeuHis 220
QY 905 ACTGGAAATGGAGCGGTTATGACACACCTGGATGCAATCTGTCCCTGGGAGACATGATGAT 964
DB 221 ThrIleMetGlnTyrArgLeuCysThrLeuAspGlnSerValSerLeuAlaThrMetIleAsp 240
QY 965 CGAATTAAGAGACACTAAACATATTCATATTCCTTACGCCCTTGGGGTGGGAGAAC 1024
DB 241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValArgThr 260
QY 1025 TTAGAGTCTCAAGTCAAAAGTCTGGGCGCTGTGCTGTGGAGCAGCGTTCTGACAG 1084
DB 261 LeuGlnSerGlnValLysValAlaIleAlaLeuCysAlaGlySerGlySerValLeuGln 280
QY 1085 GGTGTGAGCGCTGACCTTTTACCTCAGAGTGAGATGTCCTCATCATGATCTTGGATGCT 1144
DB 281 GlyValGluIubAspLeuTyrLeuThrGlyGluMetSerHisAspThrLeuAspAla 300
QY 1145 GCTTCCCAAGAAATTAATGTCATCTCTGTGACACAGACAAACATGAAAGAGCGTTCTT 1204
DB 301 AlaSerGlnGlyIleAsnValIleLeuCysGlnHisSerAsnThrGluArgGlyPheLeu 320
QY 1205 TCTGACCTTGAGATATGCTGAGATTCCTCACTTGGAGAAATTAATTAATTAATCA 1264
DB 321 SerAspLeuTyrAspMetLeuAspSerHisLeuGlnLysIleAsnIleIleLeuSer 340
QY 1265 GAGACTGACAGGAGCGCTTTCAGAGTGATA 1294
DB 341 GluThrAspArgAspProLeuGlnValVal 350

```

RESULT 4
AAB94573
ID AAB94573 standard; Protein: 350 AA.
XX
AC AAB94573;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:15360.
XX
KW Human; primer: detection; diagnosis; antisense therapy; gene therapy.
OS Homo sapiens.
XX
PN EPI074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR MPI; 2001-318749/34.

Human gene expression regulatory factor related protein and its coded
 PT sequence -
 XX
 PS Claim 4, Page 19-20; 20pp; Chinese.

XX The invention relates to a novel human gene expression regulatory
 CC factor-related protein, hNIF3-s (NGFI-interacting factor, AAB60663),
 CC and cDNA encoding it (AAFP5945). hNIF3-s is expressed in haemopoietic
 CC stem cells. The invention also relates to the preparation of hNIF3-s
 CC proteins and nucleic acids, and the detection of hNIF3-s proteins and
 CC nucleic acids in a sample. The present sequence represents hNIF3-s.

XX Sequence 351 AA:

Alignment Scores:

Pred. No.:	1,25e-165	Length:	351
Score:	1743.50	Matches:	344
Percent Similarity:	98.58%	Conservative:	2
Best Local Similarity:	98.01%	Mismatches:	4
Query Match:	62.51%	Indels:	1
DB:	22	Gaps:	1

US-09-745-506-74 (1-1553) x AAB60663 (1-351)

QY 245 ATGATTTGAAGGCTCTCTTCTCTTGAATGACTTTCATCCCTCTGTTGCTGAG 304
 DB 1 MetAspLeuLysAlaLeuLeuSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
 QY 305 AGTTGGGACAAATGTTGGATTACTGTGGACCAAGCCCACTACTAATATACACTC 364
 DB 21 SerTrpAspAsnValGlyLeuLeuValGluProSerProPheHisThrValAsnThrLeu 40
 QY 365 TTCTGTACCAATGACCTGACTGAGAGAGATGAGAGAGTCTGCAAAAGAGGACGAC 424
 DB 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysAlaAsp 60
 QY 425 CTCATTCCTCTCTACCATCCGCTATCTTCGACCCGATGAGCGCATTAACCTGG--AAC 481
 DB 61 LeuIleLeuSerTyrHisProPheIlePheArgPrometLysArgLysLeuGlnHis 80
 QY 482 ACATGGAGAGAGCGCTGATCCGGGCTCTGGAGAAAGAGTGGTATCTACTCTCT 541
 DB 81 MetGlyArgGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerPro 100
 QY 542 CATACAGCCTATGATGCTGCGCCGAGGCGTCAACAACATGCTGCTAAAGGCTTGGGA 601
 DB 101 HisThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysIleuGly 120
 QY 602 GCTGTACCTCCAGGCCCATATCATCTTCCAAAGCTCCCACTACCTCAACAGGGAAC 661
 DB 121 AlaCysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlnAsn 140
 QY 662 CACCGAGTAGAATTCACGTTTACCTACACCCCAAGACCTGGACAAAGTCTGTCAGAGC 721
 DB 141 HisAspValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaVal 160
 QY 722 AAAGGAATGACGCTGTTCTCTCACTCTTCTTTCGTCAGAGACGTCGATATSGAAGAA 781
 DB 161 LysGlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlnLysnGluGln 180
 QY 782 ACACGGATTAATCTGAATTTGACTCAGAGGCTTTGATGACAGGTGTAGATTTTCTTCC 841
 DB 181 ThrArgIleAsnLeuAsnLysThrGlnLysAlaLeuMetGlnValValAspPheLeuSer 200
 QY 842 CGGACCAAAACAATTATTCAGAGACGGAATTCGTCTACTGAGAGAGCTTTGCTTCTA 901
 DB 201 ArgAsnLysGlnLeuTyrGlnLysThrGlnIleLeuSerLeuGlnLysProLeuLeuLeu 220
 QY 902 CATACTGGAATGGAGCGGTTATGACACACTGATGATGATGCTCCCTGGACACCATGAT 961
 DB 221 HisThrGlyMetGlyArgLeuLysThrLeuAspGluSerValSerLeuAlaThrMetIle 240
 QY 962 GATCGAATTAAGAACACCTAAACTATCTCATATTCGCTTAGCCCTTGAGGTGGGAGA 1021

DB 241 AspArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArg 260
 QY 1022 ACCTTAGACTCTCAAGTCAAAAGTCCGCGCTGTGCTGTCTGGAGACAGCTTTCG 1081
 DB 261 ThrLeuGlnSerGlnValLysValAlaIleAlaCysAlaGlySerIleSerValLeu 280
 QY 1082 CAGGGGTGTAGAGCTTACCTTACCTCACAGGAGATGATCCCATCATGATCTTTGGAT 1141
 DB 281 GlnGlyValGlnAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAsp 300
 QY 1142 GCTGTCTCCCAAGGAATAATGTCATCTCTGTGACACAGCAACACTGACAGGCTTT 1201
 DB 301 AlaAlaSerGlnGlyIleAsnValIleLeuGlnLysSerAsnThrGluArgLysPhe 320
 QY 1202 CTTTGTGACCTTCGAGATATGCTGGATTTCTCACTTGGAGATTAATATATTCCTA 1261
 DB 321 LeuSerAspLeuArgAspMetLeuAspSerHisLeuGlnLysIleAsnIleIleLeu 340
 QY 1262 TCAGAGACTGACAGGAGGACCTCTTCAGTGGTGA 1294
 DB 341 SerGluThrAspArgAspProLeuGlnValVal 351

RESULT 6

AB08182
 ID ABB08182 standard; Protein; 247 AA.

XX ABB08182;

AC ABB08182; 23-SEP-2002 (first entry)

DE Human protein kinase C 27.17 polypeptide.

KX Human; protein kinase C 27.17; protein metabolism; enzyme.

OS Homo sapiens.

PN CN1333355-A.

PD 30-JAN-2002.

PF 07-JUL-2000; 2000CN-0117049.

PR 07-JUL-2000; 2000CN-0117049.

PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.

PI Mao Y, Xie Y;

DR WPI; 2002-305609/35.

DR N-PSDB; ABL60919.

XX Human protein kinase C 27.17 polypeptide and its encoding

PT polynucleotide, for treating e.g. protein metabolism disturbance -

PS Claim 1; Page 26-27 (disclosure); 33pp; Chinese.

CC The invention relates to a human protein kinase C 27.17 polypeptide and
 CC its encoding polynucleotide. The polypeptide can be expressed by standard
 CC DNA recombination. The polynucleotide, polypeptide and its antagonist are
 CC useful for treating e.g. protein metabolism disturbance. The present
 CC sequence represents the human protein kinase C 27.17 polypeptide.

XX Sequence 247 AA:

Alignment Scores:	4.32e-112	Length:	247
Pred. No.:	1209.00	Matches:	243
Score:	97.99%	Conservative:	1
Percent Similarity:	97.99%	Mismatches:	3
Best Local Similarity:	43.35%	Indels:	2
Query Match:	23	Gaps:	0

US-09-745-506-74 (1-1553) x ABB08182 (1-247)

QY 552 ATGATGCTGGCCCAAGGCGTCACACACTGTTGGCTAAAGGCTTGAGCTTGACT 611
 |||||
 Db 1 MetMetLeuArgProArgAlaSerThrThrGlyTyrLeuLysGlyLeuGluLeuValPro 20
 QY 612 CCAAGCCCAACATCTCTCCAAAGCTCCCAACTACCTACAGAGGGAACACCGAGTAG 671
 |||||
 Db 21 ProGly-HisThrSerPheGln-AlaProAsnProIlyrArgGlyThrHisArgValG 40
 QY 672 AATTCAACGTTAACTACACCAAGACCTGGACAAGATGTCGTGCGTGAAGAGATTG 731
 |||||
 Db 40 IuhPheAsnValAsnTyrThrGlnAspLeuAspIlyValMetSerAlaValLysGlyLea 60
 QY 732 ACGGTGTTCTGCTCACTCTTTCTTCAGAGCTGGTAATGAGAAACAACGAGATTA 791
 |||||
 Db 60 spGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThrArgIlea 80
 QY 792 ATCTGAATTTACTCAGAGGCTTTGATGAGGCTTGATTTTCTTCCCGGAACAAC 851
 |||||
 Db 80 snLeuAsnCystrGlnLysAlaLeuMetGlnValValaAspPheLeuSerArgAsnLysG 100
 QY 852 AACTTATCAGAGAGAGGGAATTCCTGACGTGGAGAGACCTTGTCTTACATCTGGA 911
 |||||
 Db 100 LmLeuTyrGlnLysThrGlnLleuSerLeuGluLysProLeuLeuLeuHisThrGlyM 120
 QY 912 TGGGACGGTATGACACTGGATGATGATCTGTCTCCCGCAACCATGATGATGAATA 971
 |||||
 Db 120 etGlyArgLeuCystrThrLeuAspLysSerValSerValSerLeuAlaThrMetLleAspArgIleL 140
 QY 972 AAAGACACCTAAAACATTCATATTCGCTTAGCCCTTGGGGTGGGAGAACCTTAAGT 1031
 |||||
 Db 140 ysaArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThrLeuLus 160
 QY 1032 CTCAAGCAAAAGCGTGGCCCTGTGCTGCTGCTGAGACAGCGTTCGAGGGGTGTG 1091
 |||||
 Db 160 ertGlnValLysValAlaLeuCystrAlaGlySerGlySerValLeuGlnLysValG 180
 QY 1092 AGCGTGACCTTTACCTCAGAGTGATGTCCTCCATCATATCTTGGATGCTGCTCC 1151
 |||||
 Db 180 lmlaAspLeuTyrLeuThrGlyGluMetSerHisIleAspThrLeuAspAlaIleAspG 200
 QY 1152 AAGGAATAATGTCATCTCTGTGACACAGCAACACTGGAACGAGGGTCTTCTGACC 1211
 |||||
 Db 200 lmglyIleAsnValLleuLeuCystrLysSerAsnThrGlnArgGlyPheLeuSerSPL 220
 QY 1212 TTGAGATATGCTGGATTTCTCACTTGGAGATAAGATAATATTTCTATCAGAGACTG 1271
 |||||
 Db 220 euaArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnLleIleuSerGluThrA 240
 QY 1272 ACAGGACCTCTTCAGGTGTA 1294
 |||||
 Db 240 spArgAspProLeuGlnValVal 247
 |||||
 RESULT 7
 AAU27916
 ID AAU27916 standard; Protein: 146 AA.
 XX
 AC AAU27916;
 XX
 DT 18-DEC-2001 (first entry)
 DE Human contig polypeptide sequence #69.
 DE
 XX Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
 KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
 KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
 KW nervous system disorder; inflammatory disorder; cell differentiation;
 KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
 KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
 KW cytoskeletal; antirheumatic; antiarthritic; vulnary; antiinflammatory;
 KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
 KW neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergic;

KW immunostimulant; analgesic; gene therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200164834-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04926.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 PR 17-JUN-2000; 2000US-0597707.
 PR 14-JUL-2000; 2000US-0616807.
 PR 19-SEP-2000; 2000US-0664641.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
 PI Drmanac R;
 XX
 DR WPI: 2001-589862/66.
 DR N-PSDB: AAS44816.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis, treatment of
 PT cancer, neurological, inflammatory disorders and for use in arrays for
 PT detection
 XX
 PS Claim 10; Page 132; 153pp; English.
 XX
 CC Sequences AAU27676-AAU28019 represent full-length polypeptides and
 CC contig polypeptides of the invention. The proteins and their associated
 CC DNA sequences are useful for the treatment, diagnosis and prevention of
 CC various types of disorder in a mammalian subject such as a human, dog,
 CC monkey, mouse, hamster or rat. The disorders include cancers such as
 CC leukemia, lymphoma and neuroblastoma, autoimmune disorders such as
 CC multiple sclerosis, connective tissue disease, rheumatoid arthritis,
 CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
 CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
 CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
 CC Menke disease, inflammatory disorders such as nephritis, Crohn's
 CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
 CC bowel disease. The sequences exhibit activity relating to angiogenesis,
 CC cell proliferation, cell differentiation, stem cell growth factor,
 CC activin or inhibin. Therefore, they can be used to manipulate stem cells
 CC in culture to give rise to neuroepithelial cells that can be used to
 CC augment or replace cells damaged by illness, accidental damage or genetic
 CC disorders. The sequences may also be used for regeneration of bone,
 CC cartilage, tendons and ligaments and in tissue repair and burn healing.
 CC Note: Some sequences for this patent did not form part of the printed
 CC specification, but were obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcr_sequences.
 XX
 SQ Sequence 146 AA:
 XX
 Alignment Scores:
 Pred. No.: 5,1e-51 Length: 146
 Score: 599.00 Matches: 114
 Percent Similarity: 94.53% Conservative: 7
 Best Local Similarity: 89.06% Mismatches: 7
 Query Match: 21.48% Indels: 0
 DB: Gaps: 0
 XX
 US-09-745-506-74 (1-1553) x AAU27916 (1-146)
 QY 206 TTGTGATGTTCCCGATGTCGAATTTCTTCCGCTTCATGAGATTGAAGCTCTCTCT 265
 |||||
 Db 19 PheValaAspSerLeuIleCysAsnSerArgAlaPheMetAspTPArgAlaLeuLeu 38
 |||||
 QY 266 TCTTCCTTGAMTGAAGCTTTGATCCCTCTGCTTGTGAGAGTTGGACAAAGTTGATTA 325
 |||||

Db 221 AsnaSnrHrThrValLeuLeuCyasnHisSerAsnSerGIuArgGlyPheueHnISGlu 240
QY 1211 CTTCGAGATATGCCTGGATTCTCCTTCGAGATAAAGTAATATATATCTATCAGACT 1270
Db 241 PhecysProlIleuAlaIleuAlaIleuSerIleuAsnGluIleuAlaPheValSerGIuVal 260
QY 1271 GACAGGACGCTCTTCAGGTGTA 1294
Db 261 AspIysAspProLeuValThrVal 268

RESULT 9
ABG20985
ID ABG20985 standard; Protein: 110 AA.
XX
AC ABG20985;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #20976.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS85172.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 51344; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 110 AA.
XX

Alignment Scores:

Pred. No.:	5.82e-43	length:	110
Score:	518.00	Matches:	108
Percent Similarity:	99.08%	Conservative:	0
Best Local Similarity:	99.08%	Mismatches:	1
Query Match:	18.57%	Indels:	1
DB:	22	Gaps:	0

US-09-745-506-74 (1-1553) x ABG20985 (1-110)

OY	764	ACTGGTAATGAGGAACAACACGGATTAACTGAATTGTACTGAAAGCCTTGATGACG	823
Db	2	ThrglysnnglugluginthrArgIleasnleuanscysThrGlnlysaIalaMetGln	21
OY	824	GTGGAGATTCTTCTCCCGGAACAACATTATGAGAAGACGGAATTCGTCACTG	883
Db	22	ValValasprheleuserArgasnlyscIineutyrGlnystrGlnIleleuSerIeu	41
OY	884	GAGAAACCTTTGCTTTCATACATATGGAATGGAGCGTTATGCACACTGGATGAATCTGTC	943
Db	42	GluIusProleuLeuIeuHisThrGlyMetGlyArgIeucysThrIleuAspIuSerVal	61
OY	944	TCCCTGGCAACCATGATGATGATGCAATATAAAGACACCTTAACATATGCATATTCGCTTA	1003
Db	62	SerIeuaIatmrMetIleasprArgIleIeysArgHisIeulysIeuserHisIleArgIeu	81
OY	1004	GCCCTTGGGGTGGGAGAACCTTAGAGTCTCAAGTCAAAAGTCGtGGCCCTGTGTGTGTG	1063
Db	82	AlaIeuGlyValGlyArgThrIeugIuSerIinValIysValIalaIeucyalaGly	101
OY	1064	TCTGGGAG-CAGCGTTCTGCAGGGGCT	1089
Db	102	SerGlyGluGlnArgSerAlaGlyCys	110

RESULT 10
ABG52473
ID ABG52473 standard; Peptide: 68 AA.
XX
AC ABG52473;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID NO 31121.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00664.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analysing gene expression in human adult liver -
XX
PS Claim 27; SEQ ID NO 31121; 658bp; English.
XX

CC The invention relates to a single exon nucleic acid probe (SENP) (1) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult
CC liver. (1) may be used for predicting, measuring and displaying gene
CC expression in samples derived from human adult liver. The genes
CC identified may be involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
CC is associated with coronary heart disease. ABG47348-ABG59930 represent
CC human liver single exon encoded peptides of the invention.
CC Note: The sequence information for this patent does not appear in the
CC printed specification but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 68 AA;

Alignment Scores:

Pred. No.:	7.91e-28	Length:	68
Score:	366.00	Matches:	68
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	13.12%	Indels:	0
DB:	22	Gaps:	0

US-09-745-506-74 (1-1553) x ABG52473 (1-68)

OY 395 ATGGAGAGAGTCTGCAAAAGAGGACGACCTATCTCTCCATCCGCTATCTTC 454

DB 1 MetGluGluValLeuGlnLysLysAlaAspLeuIleuSerYrHisProProlIepne 20

OY 455 CGACCATGAGGCGCATACCTGGAACACATGGAAGAGGCGCTGGTATCCGGGCTCG 514

DB 21 ArgPrometLysArgIleThrTrpAsnThrTrpLysGluArgLeuValIleArgAlaLeu 40

OY 515 GAGAACAGAGTCGGTATCTACTCTCTCATACAGCCTATGATGCTGGCCGAGGCGTC 574

DB 41 GluAsnArgValGlyIleYrSerProHisThrAlaTyrAspAlaIleProGlnGlyVal 60

OY 575 AACAACTGGTGGCTAAAGGCTT 598

DB 61 AsnAsnTrpLeuAlaLysGlyLeu 68

RESULT 11

ABR32385

ID ABR32385 standard; Peptide: 68 AA.

XX ABR32385;

XX 01-FEB-2002 (first entry)

XX Peptide #5036 encoded by breast cell single exon nucleic acid probe.

XX Human; microarray; single exon probe; gene expression; breast;

XX disease; cancer.

XX Homo sapiens.

XX MO200157271-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00662.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes,
XX useful for measuring gene expression in sample derived from human
XX breast, comprises number of single exon nucleic acid probes -

XX Claim 27; SEQ ID NO 15353; 327pp + sequence listing; English.

XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human breast and BT 474 cells. The method involves contacting
XX the probes with a collection of detectably labelled nucleic acids
XX derived from mRNA of human breast, and then measuring the label
XX bound to each probe of the microarray. The probes are useful for
XX verifying the expression of regions of genomic DNA predicted to
XX encode proteins. They are useful for gene discovery, and for
XX determining predisposition and/or prognosing breast disease. Gene
XX expression analysis is useful for assessing the toxicity of chemical
XX agents on cells. The microarray of this invention presents a far greater
XX diversity of probes for measuring gene expression, with far less bias
XX than expressed sequence tag microarrays. The method is suitable for
XX rapid production of functional information from genomic sequence. The
XX present sequence is a peptide encoded by a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 68 AA;

Alignment Scores:

Pred. No.:	7.91e-28	Length:	68
Score:	366.00	Matches:	68
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	13.12%	Indels:	0
DB:	22	Gaps:	0

US-09-745-506-74 (1-1553) x ABR32385 (1-68)

OY 395 ATGGAGAGAGTCTGCAAAAGAGGACGACCTATCTCTCCATCCGCTATCTTC 454

DB 1 MetGluGluValLeuGlnLysLysAlaAspLeuIleuSerYrHisProProlIepne 20

OY 455 CGACCATGAGGCGCATACCTGGAACACATGGAAGAGGCGCTGGTATCCGGGCTCG 514

DB 21 ArgPrometLysArgIleThrTrpAsnThrTrpLysGluArgLeuValIleArgAlaLeu 40

OY 515 GAGAACAGAGTCGGTATCTACTCTCTCATACAGCCTATGATGCTGGCCGAGGCGTC 574

DB 41 GluAsnArgValGlyIleYrSerProHisThrAlaTyrAspAlaIleProGlnGlyVal 60

OY 575 AACAACTGGTGGCTAAAGGCTT 598

DB 61 AsnAsnTrpLeuAlaLysGlyLeu 68

RESULT 12

ABR37667

ID ABR37667 standard; Peptide: 68 AA.

XX ABR37667;

XX 04-FEB-2002 (first entry)

XX Peptide #5173 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX OS

PN W0200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
DR
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
PS Claim 27; SEQ ID NO 30302; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 68 AA:

Alignment Scores:
Pred. No.: 7.91e-28 Length: 68
Score: 366.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.12% Indels: 0
DB: Gaps: 0

US-09-745-506-74 (1-1553) x ABB37667 (1-68)
OY 395 ATGAGAGAGTGTCTGCAAAAGAGCAGACCTCATCTCTCTACCATCGGCTATCTTC 454
DB 1 MetGluGluValLeuGlnLysLysAlaAspLeuIleLeuSerTyrHisProProlIlePhe 20
OY 455 CGACCCATGAAGCGCATACCTGGAACACATGAGAGAGCGCTGTGATCCGGGCTCTG 514
DB 21 ArgProMetLysArgIleThrTyrPasnThrTrpLysGluArgLeuValIleArgAlaLeu 40
OY 515 GAGAACAGAGTCGGTATCTACTCTCTCATACAGCTTGAATGCTGCGCCCGAGGGCGTC 574
DB 41 GluAsnArgValAlaGlyIleTyrSerProHisThrAlaTyrAspAlaAlaProGlnIleVal 60
OY 575 AACAACTGGTGGCTAAAGGCTT 598
DB 61 AsnAsnTrpLeuAlaLysGlyLeu 68

RESULT 13
AAM58295
ID AAM58295 standard; Protein: 68 AA.
XX
AC AAM58295;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30400.
XX

KW Human: brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN W0200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
DR
XX WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 30400; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention.
XX
SQ Sequence 68 AA:

Alignment Scores:
Pred. No.: 7.91e-28 Length: 68
Score: 366.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.12% Indels: 0
DB: Gaps: 0

US-09-745-506-74 (1-1553) x AAM58295 (1-68)
OY 395 ATGAGAGAGTGTCTGCAAAAGAGCAGACCTCATCTCTCTACCATCGGCTATCTTC 454
DB 1 MetGluGluValLeuGlnLysLysAlaAspLeuIleLeuSerTyrHisProProlIlePhe 20
OY 455 CGACCCATGAAGCGCATACCTGGAACACATGAGAGAGCGCTGTGATCCGGGCTCTG 514
DB 21 ArgProMetLysArgIleThrTyrPasnThrTrpLysGluArgLeuValIleArgAlaLeu 40
OY 515 GAGAACAGAGTCGGTATCTACTCTCTCATACAGCTTGAATGCTGCGCCCGAGGGCGTC 574
DB 41 GluAsnArgValAlaGlyIleTyrSerProHisThrAlaTyrAspAlaAlaProGlnIleVal 60
OY 575 AACAACTGGTGGCTAAAGGCTT 598
DB 61 AsnAsnTrpLeuAlaLysGlyLeu 68

RESULT 14
AAM18609
ID AAM18609 standard; Protein: 68 AA.
XX
AC AAM18609;
XX

DT 12-OCT-2001 (first entry)
XX
DE Peptide #5043 encoded by probe for measuring cervical gene expression.
XX
KW Probe: human; microarray; gene expression; cervical epithelial cell;
KM cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001MO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 27; SEQ ID NO 23435; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENs; see AAI10068-AA128459). The present sequence is a peptide encoded
CC by one such probe. The SENs are derived from human HeLa cells. The SENs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 68 AA;
XX
Alignment Scores:
Pred. No.: 7.91e-28 Length: 68
Score: 366.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.12% Indels: 0
DB: 22 Gaps: 0
XX
US-09-745-506-74 (1-1553) x AAM18609 (1-68)
QY 395 ATGAGAGAGGTGTCGAAAAGAGCGACCTCATTTCTCTACCATCCGCGCTATCTTC 454
Db 1 MetGluGluValLeuGlnLysLysAlaAspLeuIleuSerTyrHisProPhe 20
QY 455 CGACCCATGAAGCGCATACCTGGAACACATGGAAGAGCGCGTGGATCCGGGCTCTG 514
Db 21 ArgProMetLysArgIleThrPheSerThrTyrLysLysValIleArgAlaLeu 40
QY 515 GAGAACAGATCGGTATCTACTCTCTCATACACCTATGATGCTGCCGCCAGGGCTC 574
Db 41 GluAsnArgValGlyIleTyrSerProHisThrAlaTyrAspAlaIleProGlnGlyVal 60
QY 575 AACACAGTGTGGCTAAAGGCTT 598
Db 61 AsnAsnTrpLeuAlaLysGlyLeu 68

RESULT 15
AAM06178
ID AAM06178 standard; Protein: 68 AA.
XX
AC AAM06178;
XX
DT 09-OCT-2001 (first entry)
XX
DE Peptide #4860 encoded by probe for measuring breast gene expression.
XX
KW Probe: human; breast disease; breast cancer; development disorder;
KM inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001MO-US00661.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-476286/51.
XX
PT Novel single exon nucleic acid probe used to measuring gene expression
PT in a human breast -
XX
PS Claim 27; SEQ ID NO 14918; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes
CC (see AAI00010-AA110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridises at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer, disorders of development,
CC inflammatory diseases of the breast, fibrocystic changes, proliferative
CC breast disease and non-carcinoma tumours.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 68 AA;
XX
Alignment Scores:
Pred. No.: 7.91e-28 Length: 68
Score: 366.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.12% Indels: 0
DB: 22 Gaps: 0
XX
US-09-745-506-74 (1-1553) x AAM06178 (1-68)
QY 395 ATGAGAGAGGTGTCGAAAAGAGCGACCTCATTTCTCTACCATCCGCGCTATCTTC 454
Db 1 MetGluGluValLeuGlnLysLysAlaAspLeuIleuSerTyrHisProPhe 20
QY 455 CGACCCATGAAGCGCATACCTGGAACACATGGAAGAGCGCGTGGATCCGGGCTCTG 514
Db 41 GluAsnArgValGlyIleTyrSerProHisThrAlaTyrAspAlaIleProGlnGlyVal 60

Db	21	ArgProMetLysArgIleThrTrpAsnThrTriplysGluArgLeuValIleArgAlaLeu	40
QY	515	GAGAACAGAGTGGTATCTACTCTCCATACAGCCTATGATGCTGGCGCCCGAGGGCGTC	574
Db	41	GluAsnArgValGlyIleTyrSerProHisThrAlaTyrAspAlaAlaProGlnGlyVal	60
QY	575	AACAACTGGTTGGCTAAAGGCTT	598
Db	61	AsnAsnTrpLeuAlaLysGlyLeu	68

Search completed: August 22, 2003, 13:59:08
 Job time : 112 secs